

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2002, 04:47:34 ; Search time 116.57 Seconds

(Without alignments)
534.256 Million cell updates/sec

Title: US-09-719-748-2

Perfect score: 1846

Sequence: 1 MEPRKQKQVEFDYDGEELG.....TREDIARRKALHPRRRSSNS 360

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriapi:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1835	99.4	370	4	075892	075892 homo sapien
2	1824	98.8	370	4	0901K4	0901K4 homo sapien
3	1764	95.6	370	11	090YM4	090YM4 mus musculu
4	1481	80.2	303	11	088861	088861 mus musculu
5	1297	70.3	1430	11	091JP7	091JP7 mus musculu
6	1293	70.0	367	4	09BTL8	09BTL8 homo sapien
7	1251.5	67.8	345	11	09CV44	09CV44 mus musculu
8	1166	63.2	454	4	043293	043293 mus musculu
9	1140	61.8	448	11	054784	054784 mus musculu
10	1140	61.8	448	11	088764	088764 ratu
11	787	42.6	1435	5	044997	044997 caenorhabd
12	698	37.8	992	4	09C0L5	09C0L5 homo sapien
13	695	37.6	641	6	09B8E9	09B8E9 macaca fasc
14	688.5	37.3	907	13	098850	098850 carassius a
15	668.5	36.2	611	11	091XS9	091XS9 cavia porce
16	665.5	36.1	2762	5	P91255	P91255 caenorhabd

17	660	35.8	1721	5	0961U1	0961U1 drosophila
18	660	35.8	7107	5	09VAE7	09VAE7 drosophila
19	651.5	35.3	371	11	091XS8	091XS8 ratu
20	650	35.2	6658	5	076281	076281 drosophila
21	649.5	35.2	372	11	0923E7	0923E7 mus musculu
22	641	34.7	795	4	096DV1	096DV1 homo sapien
23	621.5	33.7	451	5	016980	016980 aplysia cal
24	603.5	33.7	596	4	09H1R3	09H1R3 homo sapien
25	594	32.2	577	5	09G9E1	09G9E1 drosophila
26	592	32.1	929	5	001651	001651 drosophila
27	591	32.0	732	5	09GTV1	09GTV1 drosophila
28	591	32.0	786	5	09GV79	09GV79 drosophila
29	591	32.0	832	5	001653	001653 drosophila
30	591	32.0	913	5	09V7G6	09V7G6 drosophila
31	589	31.9	1211	5	023260	023260 caenorhabd
32	586	31.7	569	5	001652	001652 caenorhabd
33	584.5	31.7	6831	5	023550	023550 caenorhabd
34	584.5	31.7	7160	5	023551	023551 caenorhabd
35	581	31.5	1289	4	09Y2A5	09Y2A5 homo sapien
36	580	31.4	2959	11	09JTF1	09JTF1 ratu
37	578.5	31.3	446	5	0958K9	0958K9 drosophila
38	571.5	31.0	335	5	061269	061269 mytilus gal
39	571.5	31.0	878	5	09GV22	09GV22 mytilus gal
40	564	30.6	357	4	09HD31	09HD31 homo sapien
41	553.5	30.0	623	5	09GV80	09GV80 drosophila
42	547	29.6	343	4	09NNY2	09NNY2 homo sapien
43	545	29.5	343	11	070150	070150 ratu
44	544.5	29.5	343	11	09QTK9	09QTK9 mus musculu
45	544	29.5	342	11	008767	008767 ratu

ALIGNMENTS

RESULT 1
ID 075892 PRELIMINARY; PRT; 370 AA.
AC 075892;
DT 01-NOV-1998 (TREMBL) 08, Created
DT 01-NOV-1998 (TREMBL) 08, Last sequence update
DT 01-DEC-2001 (TREMBL) 19, Last annotation update
DE DAP-KINASE RELATED PROTEIN 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP
RC TISSUE=KIDNEY;
RX MEDLINE=20094983; PubMed=10629061;
RA Inbal B., Shani G., Cohen O., Kissil J.L., Kinch A.;
RT "Death-associated protein kinase-related protein 1, a novel
Serine/Threonine kinase involved in apoptosis.";
RL Mol. Cell. Biol. 20:1044-1054(2000).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF052941; AAC35001.1; -
DR HSP: Q63450; IAK6.
DR InterPro: IPR00719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR APB-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 370 AA; 42923 MW; 09502B4ADC020F91 CRC64;

Query Match 99.4%; Score 1835; DB 4; Length 370;
Best Local Similarity 99.7%; Pred. No. 3.2e-125;
Matches 359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MEPRKQKQVEFDYDGEELGSGQFAIVKCKEKSTGLEYAKFKKQSRASRGVSNE 60

QY	121	KQILDGVNTHFKKLAHFDLKPENIMMLDKNIPRIKILIDFGLAHELEDOVEEKNIFGT	180
	121		
Db	131	KQILDGVNTHFKKLAHFDLKPENIMMLDKNIPRIKILIDFGLAHELEDOVEEKNIFGT	190
	131		
QY	181	PEFVAEIVNVEPLGLEADWMSIGVITYILLSGASPELDTQOETLANITSYDFDEEF	240
	181		
Db	191	PEFVAEIVNVEPLGLEADWMSIGVITYILLSGASPELDTQOETLANITSYDFDEEF	250
	191		
QY	241	FSHTSELADFTKILVETKREKLITGEALHWPITPVDOQAMVRESVNLNEMEROY	300
	241		
Db	251	FSQSELANOETIKKLVTETKRRKLTIGALRHPITPVDOQAMVRESVNLNEMEROY	310
	251		
QY	301	VRRRWKLSFVSIVLCHNLTRSLMKVYHARPEOIRNCESTFEDIARRKALPRRRSSTS	360
	301		
Db	311	VRRRWKLSFVSIVLCHNLTRSLMKVYHARPEOIRNCESTFEDIARRKALPRRRSSTS	370
	311		

36c

GN	DAPK3 OR DAPK3.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC	Kelley: Metazoa; Chordata; Vertebrata; Euteleostomi; Mus.
XX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	NB_017689:10090;
RA	[1]
RT	SEQUENCE FROM N.A.
RL	MEDLINE:99303018; PubMed-10376525;
RM	Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J.,
RJ	Jenkins N.A., Akita S.;
RH	"Death-associated protein kinase 2 is a new calcium/calmodulin-
RI	dependent protein kinase that signals apoptosis through its catalytic
RT	activity.";
RL	Oncogene 18:3471-3480(1999).
RM	-1 SIMILARITY. BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC	EMBL; AB018002; BAA88064.1; "
DR	HSSP; Q63450; 1A06.
DR	MGI: MGI:13K4129; Dapk2.
DR	InterPro: IPR000719; EuK_pkinase.
DR	InterPro: IPR002290; Ser_thr-kinase.
DR	InterPro: IPR001245; Tyr_kinase.
DR	Pfam: PF00069; pkinase.1.
DR	PRINTS: PR00109; TYRKINASE.
DR	SMART: SM00220; S_TKC.1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
DR	PROSITE: PS00108; PROTEIN_KINASE_SF.1.
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ	SEQUENCE 370 AA; 42769 MW; 7DA6E29C4E6615B3 CnC64;

Db 11 IEREVSYLROVLAHPNITLQDYENRTDVLILBVS GSELDFPLAOKSSLSSEBATSFI
QY 61 IEREVSYLROVLAHPNITLQDYENRTDVLILBVS GSELDFPLAOKSSLSSEBATSFI
Db 71 IEREVSYLROVLAHPNITLQDYENRTDVLILBVS GSELDFPLAOKSSLSSEBATSFI
QY 121 KQILDGVNNTLTATKRIAHFDLKPENIMLDLDRKNIPRPHIKLIDFGIAHEIEDGVFEKNISFT
Db 131 KQILDGVNNTLTATKRIAHFDLKPENIMLDLDRKNIPRPHIKLIDFGIAHEIEDGVFEKNISFT

ID	043293	PRELIMINARY;	PRT;	454 AA.
AC	043293;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)			
DE	ZTP-KINASE.			
CN	ZTPK.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98147805; PubMed=9488481;			
RA	Kawai T., Matsumoto M., Takeda K., Sanjo H., Akira S.;			
RT	"ZTP kinase, a novel serine/threonine kinase which mediates			
RT	apoptosis".			
RL	Mol. Cell. Biol. 18:1642-1651(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99283879; PubMed=10356987;			
RA	Muraie-Hori M., Suizu F., Iwasaki T., Kikuchi A., Hosoya H.;			
RT	"ZTP kinase identified as a novel myosin regulatory light chain kinase			
RT	in HeLa cells.";			
RL	FEBS Lett. 451:81-84(1999).			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR	EMBL; AB007144; BAA24955.1; -			
DR	EMBL; AB022341; BAA81746.1; -			
DR	HSSP: O63450; 1A06.			
DR	InterPro: IPR000729; Euk_pkinase.			
DR	InterPro: IPR002290; Ser_Thr_pkinase.			
DR	Pfam: PF00069; pkinase; 1.			
DR	SMART: SM00220; S_TKC; 1.			
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE: PS5011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.			
DR	ATP-binding_Kinase_Serine/Threonine-protein kinase; Transferase.			
KW	SEQUENCE 454 AA; 5253 MW; 56773008A6A61Cf0 CRC64;			

[illegible]

AC 054784; 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ZIP-KINASE.
 GN DAPK3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96147805; Pubmed=9488481;
 RA Kawai T., Matsumoto M., Takeda K., Sanjo H., Akita S.;
 RT "ZIP-kinase, a novel serine/threonine kinase which mediates
 RT apoptosis.";
 RL Mol. Cell. Biol. 18:1642-1651(1998).
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB007143; BAA24954.1; -.
 DR HSSP: Q63450; IA06.
 DR MGD: MGI:1203520; Dapk3.
 DR InterPro: IPR000719; Ser_thr_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_Trc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase
 SQ SEQUENCE 448 AA; 51421 MW; DM3J2EF3E51F70EFC CAC64;

Query Match	Similarity	61.8%	Score 1140:	DB 11:	length 448:
Best Local	Similarity	71.0%	Pred. No. 9.7e-75:		
Matches	225:	Conservative	38:	Mismatches	42:
				Indels	12:
				Gaps	2:
QY	1	MEPFKQAKVEDYDYGEGELSGGOFALVKKCRCKSTGLEAAAFIKKRQSRASRGVSRRE	60		
DB	1	MEPFQGEDEVEDYHMEGSELGGGPAIVRKCQCKGKGMEAAAFIKKRRLPSSRGVSRRE	60		
QY	61	IRREVSILRQVYLHHNVITLADYENRNDVYHILELVSGGELDFDLAQKSLSEERATSTI	120		
DB	61	IRREVSILRKHHPNITLHDYFENKTDVYLILELVSGGELDFDLAEKESLDEDEATOPTL	120		
QY	121	KOILGVNVLHRRKTLIAHFDLPKPEINMLDKNPIPIKTLIDRGLAHEITDGVGFNNIFET	180		
DB	121	KOILGVNVLHRRKTLIAHFDLPKPEINMLDKHAAAPRIKTLIDRGLAHEITDGVGFNNIFET	180		
QY	181	PEFVAPEIYNYEPLGLHADMSIGVITYILLGSASPFLGDTQOETLANITSYSDFDEEF	240		
DB	181	PEFVAPEIYNYEPLGLHADMSIGVITYILLGSASPFLGDTQOETLANITSANYPDEDEY	240		
QY	241	FSEHTELANQDITRKLILVYKTRKRLITIOEALRHPWITPVNDQOAMVRESVNLLENFRQY	300		
DB	241	FESTSELANQDITRKLILVYKTRKRLITIOEALRHPWITPVNDQOAMVRESVNLLENFRQY	300		
QY	301	VRRMKLSFSVSLCNH 317			
DB	289	RRRLRAARLREYSLSKSH 305			
RESULT	10				
ID	088764	PRELIMINARY:	PRT:	448 AA.	
AC	088764:				
DT	01-NOV-1998 (TREMBlrel. 08, Created)				
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)				
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)				
GN	DAP-LIKE KINASE.				
DE					
OS	Rattus norvegicus (rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				

OX NCBI_TaxId=10116;
 RN SEQUENCE FROM N.A.
 RP Kogel D., Plotter O., Landsberg G., Christian S., Scheidtmann K.:
 RT "Cloning and characterisation of DLK, a novel serine/threonine kinase
 RT that is tightly associated with chromatin and phosphorylates core
 RT histones.";
 RL Oncogene 20:2645-2654(1998).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF006971; CA07360.1; .
 DR HSSP: 063450; 1A06.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 448 AA; 51449 MW; 8430FDD0BF0C1EEA CRC64;

Query Match 61.8%; Score 1140; DB 11; Length 448;

Best Local Similarity 71.0%; Pred. No. 9.7e-75; Indels 12; Gaps 2;

Matches 225; Conservative 38; Mismatches 42;

OY 1 MEPPKQKQVDFPDIGELSGQFAIVKCKREKSTGLEVAAKFKRKRSRSGVSRRE 60
 DB 1 MSTRFQDVEHHEMGELOSQGFALVRKQCKGTGMEVAKFIKKRRRLPSSRRGVSRRE 60
 OY 1 IEREVSILROYLHNHNTLHDVYENRTDVVHILEVSGGELFPLAKOKESLSEETSPF 120
 DB 1 IEREVSILREIRHNITLHDVFNKTDVLLILEVSGGELFPLAKESLTDEDTQFL 120
 OY 121 KQIIDGVNYLHTKRIAHFDLKPENIMLDKNIPRIKILDFGLAHEIDGVFEKNIFFT 180
 DB 121 KQIIDGVNYLHSHKRIAHFDLKPENIMLDKNIAASPRILKIDFGIAHIEAGSEFKNFFGT 180
 OY 181 PEFAVPELVNTEPLGLEADMSIGVITYILSGASPLGDTKQETLANITSVSYDPEDEF 240
 DB 181 PEFAVPELVNTEPLGLEADMSIGVITYILSGASPLGDTKQETLANITSVSYDPEDEF 240
 OY 241 FSHSEELKQDFRKLIVETKRLITIOALRHPWITPYDNOQAMVRESVYNLENFRKQY 300
 DB 241 FSTSELKADDFRLKLVADPKRKMTIAGSLSHSWT-----KYRRRE---DGARKPE 288
 OY 301 VRRRWKLSFYSVLCNH 317
 DB 289 RRRRLRAARLREYSLKSH 305

RESULT 11
 O44997 PRELIMINARY; PRT; 1435 AA.

ID O44997;
 AC O44997;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE K12C11.4 PROTEIN.
 GN K12C11.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Wamsley P., Kramer J.;
 RT "The sequence of C. elegans cosmid K12C11.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF043701; AAK18971.1; .
 DR HSSP: 063450; 1A06.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00023; ank; 7.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR SMART: SM00088; ANK_REPEAT; 7.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ANK repeat; ATP-binding; Repeat; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1435 AA; 160602 MW; C73EB605C37FB732 CRC64;

Query Match 42.6%; Score 787; DB 5; Length 1435;

Best Local Similarity 47.9%; Pred. No. 1.7e-48; Indels 6; Gaps 4;

Matches 160; Conservative 63; Mismatches 105;

OY 22 GQFAIYKCKREKSTGLEVAAKFKRKRSRSGVSRREIEREVSILROYL-HNHVITLH 80
 DB 80 GQFAVVRARVDRDKTGKGVAAKFIKKRVATSRGVTQWIEIEVVLKIRGNSVNVLEH 139
 OY 81 DYVENRTDVVHILEVSGGELFPLAKOKESLSEETSPFQIIDGVNYLHTKRIAHFDL 140
 DB 140 AVEETASDVYIIVLELVSGGELFDHVCACKCLDEVEAAATIKQILLAVRLHSLHVIDI 199
 OY 141 KPEINIMLDKNIPRIKILDFGLAHEIDGVFEKNIFFTPEFAVPELVNTEPLGLEADM 200
 DB 200 KPEINIML--KQGDSDIKITIDFSLREIEGAVKDMVGTPEFAVPELVNTEPLSPATDM 257
 OY 201 WSGIVITYILSGASPLGDTKQETLANITSVSYDDEEFSTSELAKDFIRKLIVKET 260
 DB 258 WAGGVVITYILSGSPFLGDNROETFSNITVRHFSDFKNTSKHANDFIYRLVFDV 317
 OY 261 RKRLTIOALRHPWITPYDNOQAMVRESVYNLENFRKQYVRRRWKLSFYSVLCNHLR 320
 DB 318 DQRAVTECLQHPWIRPBGNAIDIRKASCITTSIHGFSFTRBWRKVCVELVYVLKASK 377
 OY 321 SLARKVHLRPDED--LRNCESDTEEDTARKKALH 352
 DB 378 SSRRIQGRFDEEDMVASCTLCAEE-GNLRALH 410

RESULT 12
 G9C0L5 PRELIMINARY; PRT; 992 AA.

ID G9C0L5;
 AC G9C0L5;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYOSIN LIGHT CHAIN KINASE.
 GN MLCK.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query Match	37.8%	Score 698	DB 4	Length 992
Best Local Similarity	41.6%	Pred. NO. 3e-42		
Matches 146	Conservative 66	Mismatches 117	Indels 22	Gaps 6

RESULT	ID	PRELIMINARY:	PRT:	641 AA.
13	Q9BE69			
	Q9BE69			
AC	Q9BE69			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	HYDROTHERICAL 72.2 KDA PROTEIN.			
	Macaca fascicularis (Crib eating macaque) (Cynomolgus monkey)			

Query Match	37.6%	Score 695	DB 6	Length 641
Best Local Similarity	41.6%	Pred. No. 2.8e-42		
Matches 146	Conservative 65	Mismatches 118	Indels 22	Gaps 6

RESULT	14	
098850		
ID	098850	PRELIMINARY:
AC	098850:	PRT: 907 AA.
DT	01-FEB-1997	(TREMBlrel, 02, Created)
DT	01-FEB-1997	(TREMBlrel, 02, Last sequence update)

```

01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE MYOSIN LIGHT CHAIN KINASE (FRAGMENT).
GN MICK.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BASEAL ARTERY;
RA Nakamura A., Liu L., Hanyuda Y., Kohama K.;
RT "Molecular cloning of myosin light chain kinase of the cells derived
   from Guinea pig vascular smooth muscle."
   Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AB070227; BAB63286.1; -.
KW Kinease.
KW NON_TER
FT FT
SQ SEQUENCE 611 AA; 68810 MW; 14B6EF874BB6A7F5 CRC64;

Query Match 36.2%; Score 668.5; DB 11; Length 611;
Best Local Similarity 44.2%; Pred. No. 2, 2e-40;
Matches 134; Conservative 56; Mismatches 98; Indels 15; Gaps 5

QY 6 QOKVEDFYDIGELSGQFAIVKCKCREKSTGLEVAKFIKKRQSRASRGVSREREIEV 65
DB 316 EKKVSDLYDIEERLGSQKFGQVFLVRKLEKTIWAKGFFKAVSAK-----EKENIRMEI 369
QY 66 SLROYLHNHVITLHDVYENRTDVAHILELVSGGELFDEFLAQKE-SLSPREATSFRIK 124
DB 370 GIMNCLHHRKLVOCVDAFEERKANIVMLETVSGGELFERLIDEDFELTRERCIQYMRQIS 429
QY 125 DGVNYYLTKIKIAHFLDKPENIMLDKRNIPRIKILIDFGLAHEIDEGVEFFKNIFGTPFEV 184
DB 430 EGVEYIHKQIVLHDLKPENIMCVNKT--GTRIKLIDFGLARLENAGSLKVLFGTPFEV 487
QY 185 APEIVNEPRLGLEADMSIGVITYTLLSGASPFIGDTRKQETLANITSVSYPDEEFFSHT 244
DB 488 APEVINEPFGVATDMSIGVICYLVSGLSPFMGDNDDEFLANVTSATWDFDEAFDEI 547
QY 245 SELAKDRIKLVLKETRKRLLTQELARHPWI--TPVNDQAAVRRRESVYNLENRKOYVR 303
DB 548 SEDAKDITSNMLKKDKMKNRNLNCTECIQHPMLMKDTKNMEA----KRLSKDRMKITMARR 602
QY 304 RWK 306
DB 603 KWO 605

Search completed: May 18, 2002, 05:11:43
Job time: 1449 sec

```


Sat May 18 15:09:09 2002

us-09-719-748-2.rspt

This Page Blank (uspto)